1/35
SEQUENCE LISTING

5	<110>	Biot Pfiz Gais	er I	nc		gy L	imit	ed							
	<120>	Poly	keti	des	and	thei	r sy	nthe	sis						
10	<130>	IP00	13-W	001											
10	<150> <151>	GB03 2003													
15	<160>	57													
13	<170>	Pate	ntIn	ver	sion	3.2									
20	<210> <211> <212> <213>	1 305 PRT Stre	ptom	yces	fra	diae									
	<400>	1													
25	Met As 1	n Asp	Arg	Pro 5	Arg	Arg	Ala	Met	Lys 10	Gly	Ile	Ile	Leu	Ala 15	Gly
30	Gly Se	r Gly	Thr 20	· Arg	Leu	Arg	Pro	Leu 25	Thr	Gly	Thr	Leu	Ser 30	Lys	Gln
35	Leu Le	u Pro 35	Val	Tyr	Asp	Lys	Pro 40	Met	Ile	Tyr	Tyr	Pro 45	Leu	Ser	Val
	Leu Me 50	t Leu	Ala	Gly	Ile	Arg 55	Glu	Ile	Gln	Ile	Ile 60	Ser	Ser	Lys	Asp ·
40	His Le 65	u Asp	Leu	Phe	Arg 70	Ser	Leu	Leu	Gly	Glu 75	Gly	Asp	Arg	Leu	Gly 80
45	Leu Se	r Ile	Ser	Tyr 85	Ala	Glu	Gln	Arg	Glu 90	Pro	Arg	Gly	Ile	Ala 95	Glu
50	Ala Ph	e Leu	Ile 100	Gly	Ala	Arg	His	Ile 105	Gly	Gly	Asp	Asp	Ala 110	Ala	Leu
55	Ile Le	u Gly 115	Asp	Asn	Val	Phe	His 120	Gly	Pro	Gly	Phe	Ser 125	Ser	Val	Leu
	Thr Gl	y Thr O	Val	Ala	Arg	Leu 135	Asp	Gly	Cys	Glu	Leu 140	Phe	Gly	Tyr	Pro
60	Val Ly	s Asp	Ala	His	Arg	Tyr	Gly	Val	Gly	Glu	Ile	Asp	Ser	Gly	Gly

PCT/GB2004/005001 WO 2005/054265

2/35 160 155 145 150

Arg Leu Leu Ser Leu Glu Glu Lys Pro Arg Arg Pro Arg Ser Asn Leu 5 170 Ala Val Thr Gly Leu Tyr Leu Tyr Thr Asn Asp Val Val Glu Ile Ala 10 Arg Thr Ile Ser Pro Ser Ala Arg Gly Glu Leu Glu Ile Thr Asp Val 195 15 Asn Lys Val Tyr Leu Glu Gln Gly Arg Ala Arg Leu Thr Glu Leu Gly 215

Arg Gly Phe Ala Trp Leu Asp Met Gly Thr His Asp Ser Leu Leu Gln 20 230

Ala Gly Gln Tyr Val Gln Leu Leu Glu Gln Arg Gln Gly Glu Arg Ile 25 245 250

Ala Cys Ile Glu Glu Ile Ala Met Arg Met Gly Phe Ile Ser Ala Glu 265

Gln Cys Tyr Arg Leu Gly Gln Glu Leu Arg Ser Ser Ser Tyr Gly Ser 275

35 Tyr Ile Ile Asp Val Ala Met Arg Gly Ala Ala Ala Asp Ser Arg Ala 295

40 Gln 305

30

<210> 2 <211> 303 45 <212> PRT <213> Streptomyces fradiae

<400> 2

50 Met Asn Asp Arg Pro Arg Arg Ala Met Lys Gly Ile Ile Leu Ala Gly

Gly Ser Gly Thr Arg Leu Arg Pro Leu Thr Gly Thr Leu Ser Lys Gln 55 20

Leu Leu Pro Val Tyr Asp Lys Pro Met Ile Tyr Tyr Pro Leu Ser Val 40 60 35

3/35

PCT/GB2004/005001

	Leu	Met 50	Leu	Ala	Gly	Ile	Arg 55	Glu	Ile	Gln	Ile	Ile 60	Ser	Ser	Lys	Asp
5	His 65	Leu	Asp	Leu	Phe	Arg 70	Ser	Leu	Leu	Gly	Glu 75	Gly	Asp	Arg	Leu	Gl <sub>3</sub> 80
10	Leu	Ser	Ile	Ser	Tyr 85	Ala	Glu	Gln	Arg	Glu 90	Pro	Arg	Gly	Ile	Ala 95	Glu
15	Ala	Phe	Leu	Ile 100	Gly	Ala	Arg	His	Ile 105	Gly	Gly	Asp	Asp	Ala 110	Ala	Let
20	Iļe	Leu	Gly 115	Asp	Asn	Val	Phe	His 120	Gly	Pro	Gly	Phe	Ser 125	Ser	Val	Leu
	Thr	Gly 130	Thr	Val	Ala	Arg	Leu 135	Asp	Gly	Cys	Glu	Leu 140	Phe	Gly	Tyr	Pro
25	Val 145	Lys	Asp	Ala	His	Arg 150	Tyr	Gly	Val	Gly	Glu 155	Ile	Asp	Ser	Gly	Gly 160
30	Arg	Leu	Leu	Ser	Leu 165	Glu	Glu	Lys	Pro	Arg 170	Arg	Pro	Leu	Glu	Pro 175	Gly
35	Arg	His	Arg	Leu 180	Tyr	Leu	Tyr	Thr	Asn 185	Asp	Val	Val	Glu	Ile 190	Ala	Arg
10	Thr	Ile	Ser 195	Pro	Ser	Ala	Arg	Gly 200	Glu	Leu	Glu	Ile	Thr 205	Asp	Val	Asn
	Lys	Val 210	Tyr	Leu	Glu	Gln	Gly 215	Arg	Ala	Ala	His	Gly 220	Ala	Gly	Ala	Val
15	Val 225	Ala	Trp	Leu	Asp	Met 230	Gly	Thr	His	Asp	Ser 235	Leu	Leu	Gln	Ala	Gly 240
50	Gln	Tyr	Val	Gln	Leu 245	Leu	Glu	Gln	Arg	Gln 250	Gly	Glu	Arg	Ile	Ala 255	Cys
i5	Ile	Glu	Glu	Ile 260	Ala	Met	Arg	Met	Gly 265	Phe	Ile	Ser	Ala	Glu 270	Gln	Cys
<b>60</b>	Tyr	Arg	Leu 275	Gly	Gln	Glu	Leu	Arg 280	Ser	Ser	Ser	Tyr	Gly 285	Ser	Tyr	Ile

4/35

Ile Asp Val Ala Met Arg Gly Ala Ala Ala Asp Ser Arg Ala Gln 290 295 300

5	<210 <211 <212 <213	> 3 > E	33 R <b>T</b>	tomy	ces	frad	iae									
10	<400	> 3	3													
	Met 1	Arg	Val	Leu	Val 5	Thr	Gly	Gly	Ala	Gly 10	Phe	Ile	Gly	Ser	His 15	Phe
15	Thr	Gly	Gln	Leu 20	Leu	Thr	Gly	Ala	Tyr 25	Pro	Asp	Leu	Gly	Ala 30	Thr	Arg
20	Thr	Val	Val 35	Leu	Asp	Lys	Leu	Thr 40	Tyr	Ala	Gly	Asn	Pro 45	Ala	Asn	Leu
25	Glu	His 50	Val	Ala	Gly	His	Pro 55	Asp	Leu	Glu	Phe	Val 60	Arg	Gly	Asp	Ile
30	Ala 65	Asp	Gln	Ala	Leu	Val 70	Arg	Arg	Leu	Met	Glu 75	Gly	Val	Gly	Leu	Val 80
	Val	His	Phe	Ala	Ala 85	Glu	Ser	His	Val	Asp 90	Arg	Ser	Ile	Glu	Ser 95	Ser
35	Glu	Ala	Phe	Val 100	Arg	Thr	Asn	Val	Glu 105	Gly	Thr	Arg	Val	Leu 110	Leu	Gln
40	Ala	Ala	Val 115	Asp	Ala	Gly	Val	Gly 120	Arg	Phe	Val	His	Ile 125	Ser	Thr	Asp
45	Glu	Val 130	Tyr	Gly	Ser	Ile	Ala 135		Gly	Ser	Trp	Pro 140	Glu	Asp	His	Pro
50	Leu 145	Ala	Pro	Asn	Ser	Pro 150	Tyr	Ala	Ala	Thr	Lys 155		Ala	Ser	Asp	Leu 160
	Leu	Ala	Leu	Ala	Tyr 165	His	Arg	Thr	Tyr	Gly 170		Asp	Val	Arg	Val 175	Thr
55	Arg	Cys	Ser	Asn 180		Tyr	Gly	Pro	Arg 185		Tyr	Pro	Glu	Lys 190		Val
60	Pro	Leu	Phe 195		Thr	Asn	Leu	Leu 200		Gly	Leu	Pro	Val 205		Leu	Tyr

5/35

WO 2005/054265 PCT/GB2004/005001

5	Gly Asp G	ly Gly As	n Thr A	Arg Glu 215	Trp Leu	His Val		Asp	His	Cys
	Arg Gly Va 225	al Ala Le	u Val A 230	Ala Ala	Gly Gly	Arg Pro	Gly	Val	Ile	Tyr 240
10	Asn Ile G	y Gly Gl	y Thr G 5	Glu Leu	Thr Asn 250	Ala Glu	ı Leu	Thr	Asp 255	Arg
15	Ile Leu G	u Leu Cy: 260	s Gly A	Ala Asp	Arg Ser 265	Ala Val	Arg	Arg 270	Val	Ala
20	Asp Arg Pr 27	o Gly His	s Asp A	Arg Arg 280	Tyr Ser	Val Asp	Thr 285	Thr	Lys	Ile
25	Arg Glu Gl 290	u Leu Gly	y Tyr A 2	ala Pro	Arg Thr	Gly Ile		Glu	Gly	Leu
	Ala Gly Th	r Val Ala	Trp T	'yr Arg	Asp Asn	Arg Ala 315	Trp	Trp	Glu	Pro 320
30	Leu Lys Ar	g Ser Pro 325	Gly G	ly Arg	Glu Leu 330	Glu Arg	Ala			
35	<210> 4 <211> 333 <212> PRT <213> Str	eptomyces	fradia	ae						
40	<400> 4									
4.5	Met Arg Va 1	l Leu Val 5	Thr G	ly Gly	Ala Gly 10	Phe Ile	Gly		His 15	Phe
45	Thr Gly Gl	n Leu Leu 20	Thr G		Tyr Pro 25	Asp Leu		Ala : 30	<b>Thr</b>	Arg
50	Thr Val Va.	l Leu Asp	Lys Le	eu Thr ' 40	Tyr Ala	Gly Asn	Pro 2	Ala A	Asn	Leu
55	Glu His Va	l Ala Gly	His Pr 55	ro Asp 1 5	Leu Glu	Phe Val 60	Arg (	Gly <i>F</i>	Asp	Ile
50	Ala Asp His	Gly Trp	Trp Ar	rg Arg 1		Glu Gly 75	Val (	Gly I		Val 80

										6/3	15					
	Val	His	Phe	Ala	Ala 85	Glu	Ser	His	Val	Asp 90	Arg	Ser	Ile	Glu	Ser 95	Ser
5	Glu	Ala	Phe	Val 100	Arg	Thr	Asn	Val	Glu 105	Gly	Thr	Arg	Val	Leu 110	Leu	Gln
10	Ala	Ala	Val 115	Asp	Ala	Gly	Val	Gly 120	Arg	Phe	Val	His	Ile 125	Ser	Thr	Asp
15	Glu	Val 130	Tyr	Gly	Ser	Ile	Ala 135	Glu	Gly	Ser	Trp	Pro 140	Glu	Asp	His	Pro
	Val 145	Ala	Pro	Asn	Ser	Pro 150	Tyr	Ala	Ala	Thr	Lys 155	Ala	Ala	Ser	Asp	Leu 160
20	Leu	Ala	Leu	Ala	Tyr 165	His	Arg	Thr	Tyr	Gly 170	Leu	Asp	Val	Arg	Val 175	Thr
25	Arg	Cys	Ser	Asn 180	Asņ	Tyr	Gly	Pro	Arg 185	Gln	Tyr	Pro	Glu	Lys 190	Ala	Val
30	Pro	Leu	Phe 195	Thr	Thr	Asn	Leu	Leu 200	Asp	Gly	Leu	Pro	Val 205	Pro	Leu	Tyr
35	Gly	Asp 210	Gly	Gly	Asn	Thr	Arg 215	Glu	Trp	Leu	His	Val 220	Asp	Asp	His	Cys
40	Arg 225	Gly	Val	Ala	Leu	Val 230	Gly	Ala	Gly	Gly	Arg 235	Pro	Gly	Val	Ile	Tyr 240
40	Asn	Ile	Gly	Gly	Gly 245	Thr	Glu	Leu	Thr	Asn 250	Ala	Glu	Leu	Thr	Asp 255	Arg
45	Ile	Leu	Glu	Leu 260	Cys	Gly	Ala	Asp	Arg 265	Ser	Ala	Leu	Arg	Arg 270	Val	Ala
50	Asp	Arg	Pro 275	Gly	His	Asp	Arg	Arg 280	Tyr	Ser	Val	Asp	Thr 285	Thr	Lys	Ile
55	Arg	Glu 290	Glu	Leu	Gly	Tyr	Ala 295	Pro	Arg	Thr	Gly	Ile 300	Thr	Glu	Gly	Leu
	Ala 305	Gly	Thr	Val	Ala	Trp 310	Tyr	Arg	Asp	Asn	Arg 315	Ala	Trp	Trp	Glu	Pro 320
50	Leu	Lys	Arg	Ser	Pro	Gly	Gly	Arg	Glu	Leu	Glu	Arg	Ala			

7/35 325 330

<210> 5 5 2160 DNA Streptomyces eurythermus <400> 5 10 ggcatgcctt cggggtgtgc ggcggcgcct cagagcgtgg ccagtacctc gtgcagggcc 60 gegateacet tgteetgtae gtegggegeg ageecegggt acateggeag egagaagate 120 tegteegeea geegeteegt caceggeage gageeettgg egtaceeeag gtgegegaag 180 15 cccgtcatgg tgtgcacggg ccacgggtaa ctgatgttga gcgagatccc gtacgacttg 240 agegeetega tgatgtegte eeggegeggg tggeggaega egtacaegta atacaegtgg 300 20 tegttgeeet eggtgaegga eggeageace aggeegeegg ggeeegteag gttegegagt 360 cetteggegt aacgeeggge gacegegege eggeeetega tgtageggte gaggegggtg 420 agettgegge geaggatete egeetgeace tegtegagee ggetgttgtg geegggegte 480 25 tgcacgacgt agtacacgtc ctccatgccg tagtagcgca gccggcgcag cgcacggtcg 540 acgtccgcgt cgtcggtcag cacggccccg ccgtcgccgt acgcaccgag gaccttcgtc 600 30 gggtagaacg agaaggcggc ggcgtcgccc agcgtgccgg ccagctcgcc gtggtggcgg 660 geacegtgeg cetgggegea gteeteeage accaecagge egtgetgete ggeeagggeg 720 780 egeaagggeg ceatgtegae geactgeeeg tacaggtgea ceggeageag ggeettegtg 35 cgcggggtga tgacgtccgc gacctggtcg gtgtccatga ggtggtcctc ggcgcggacq 840 tegaegaaga egggegtgge aceggtgeeg tegatggeea ceaeegtegg egeggeegtg 900 40 ttggagacgg tgacgacctc gtcccccggg cccaccccga gcgcctgcag acccagcttg 960 acggcgttgg tgccgttgtc gacaccgccg cagtggcgca ggccgtggta gtccgcgaac 1020 tccttctcga acccgtccac gctggggccg aggaccaact gcccggaggc gaagacggtc 1080 45 tegacggegt egaggaggte egegegtteg ttetggtatt eegecaggta gteecagaeg 1140 taggtagtca cggagagctc aacctccaga gtgtttcgat ggggtggtgg gaagccggtg 1200 50 egegeggace aggtegtgee ageagtegeg gacegactee egeagegaae ggegeggtge 1260 ccagcccage agggcgcgcg ccgcgccggt gtcgacccgc agccagtcct cccggtgccc 1320 gggagecegg eeeggageeg ggegeteeac caeeegegee ggaatgeege tegeetegat 1380 55 gaacaggccg accaggtcgc ggacggcgac cgcctcgccc cgcccgatgc cgacggcgac 1440 egggaeggee ggtgegeggg eggeggeeac gaeggegteg geeaegteec geacategae 1500 60 gtagtecegg tgegegegea geegggaeag ttecaegaeg geeteegeae eegteeegge 1560

				0/33			
	ggccgccagc	agccgctcgg	cgacctggcc	cagcagactg	atccgcgggg	tgccggggcc	1620
	cgacacgttg	gacacccgta	gcaccacacc	gtcgacccac	ccgcccgagg	tgccccgcag	1680
5	caccgcctcg	ctggcggcga	gcttgctcct	gccgtacgcc	gtgtccgggc	gcggtacggc	1740
	gtcggcgccc	accgaaccgc	cgggcgtcac	cgggccgtac	tccagtaccg	agccgaggtg	1800
10	gaccagccgc	ggccgcgcgg	acatcagcgc	cagcgcctcc	agcaggcgca	gcgtgggcac	1860
	cgcggtggcg	gaccacatet	gctcgtcggt	acggccccag	atgcttccga	cggagttgac	1920
	gatcgtgtcc	ggacgctccg	cgtccagggc	ggcggccagc	gccgcgggat	ccgtaccggc	1980
15	caggtccagg	gtgacgcagc	ggtacggcat	cggctcctcg	ggcgggcggc	ggcccaccac	2040
	caccacgtca	eggeeeegeg	cggcgaacgc	cgcgcacaca	tgccggccga	cgtacccggc	2100
20	gccgcccagg	accacgacgc	tgccactgcc	actgccgcgc	ggcatcggat	cgttcaccat	2160
25	<210> 6 <211> 446 <212> DNA <213> Stre	1 eptomyces en	ırythermus				
	<400> 6 cgtcagtaca	gcgtgtgggc	acacgccacc	agggtgcgca	gctcgatgtt	gaggtagttg	60
30	ccgtgcgcca	gcagcccggt	gagctgaccg	agcgacagcc	aggcgaagtc	gtccggtgcg	120
	tcctccggga	agtcgtgcgg	gacctccacg	atcacgtagc	ggttctgggc	gtggaagaag	180
35	cgcccgccct	cctcggactg	gacggcgtcg	tagcgcacgt	cctgaggcgg	cgcggacagc	240
33	acgtcctcca	ggtacggcgg	gccgggcagc	ccccgcggac	cggtgtgctc	ctgtggccgg	300
	cactggaccg	tgggggccag	ctcggcgacg	ttcaggtgcc	cgacgtccac	ccgtgcccgc	360
40	acgagcgcgt	gcagcacgcc	gtcgacggac	ttgaccagca	gcgccatcag	acccggcagc	420
	cgcggctcga	tgagcggctg	cgtccaggag	gtgacctccc	ggctgctggc	gctgacctcg	480
45	gcggccatga	cccggaagtg	ccgcccgctc	tcgtgggcga	tctcgtgcgg	cgtgcggtac	540
	cagccgtccg	ccgtcaccgt	atcgagcggc	acccggttct	gcaccagctc	ccgcagggcg	600
	cgcacacccg	tgaaccacgt	caggacctcg	gccgtcatgt	gccgcgccgc	acccggcgag	660
50	ccgaagaagg	agcgcagcac	gggggacggg	gcggacgcgt	cggcgtccgc	cgtgggcagg	720
	caggcgagga	tggaccgggc	gtccatgttg	accacgttgt	ccagcatcag	cagccggcgg	780
55	agctgcccca	gcgtcagcca	gcggaagtcc	tccccgatgt	cgaggtcgtc	gtccgccgcc	840
	aactcgacga	tcatgttccg	gttgcgtttg	gccaggaacc	agtccgcctg	ttcggactgg	900
	atcgagtcga	ccaggacacg	cgcccgtcgc	ggccccatga	acaggtccag	atagcggatg	960
60	tcgcgccccc	ggtgcacccc	ggtgaagttg	ctccgggtgg	cctgcacggt	cggcgacacc	1020

9/35

tgaagaacgt tgacgttccc gggctccatc ttggcctgca tcaggaagtg cagcacccg 1080 tcgatctccc gcgccacgat cccgagcagc cccacctccg gctgcacgat gatgggctgc 1140 5 1200 gtccagcccc gctcgggcag ccggtccgta cggacgtgca gcccctccac ggagaagaaa cggcccgacg cgtggtgcag gtttcccgta cccgggtgga agctccagcc gcgcagctcc 1260 gcgaagggaa cgcgggacac gtcgaagcgc cccgcccgca ggcgttcggc cagccagccg 1320 10 gagatgccgt cgaacggcgt gaccgcactg tccgcggtgc gtgccgacac cagcacccgc 1380 egegeegtgt ceaeegggte aeegggeegg aeegegteeg eaeggegeeg egeggeeg 1440 15 tgcggggcgg gggcggatcg cggcggtacg ggttcgcggg cggtgtccgc ggcggtgcgc 1500 ggcgggacgg ggccggtgct cgtgtccgcg gcggtacgcg gtgggacggt cccggtggcc 1560 gtgtccgcgg tggccgtgcc ggcgagggcg tcgccgatgg tccggcacac ctcgtccatc 1620 20 eggtegttea gatagaagtg acegeeggeg aaggtgtgea gggegaaggg geeegtggte 1680 agctcccgcc aggccctcgc ctcctccagc gggacatcgg gatcacggtc accggtgagc 1740 25 accgtgaccg gacagtccag cgcaccgccg ggcacatacg cgtacgtgcc cgccgcccgg 1800 tagtcgttgc ggatcgccgg cagggccagc cgcagcagct cctcgtcctg gaggacggcg 1860 tecteggtge cetgaagegt ggegatetee gegateageg egtegtegte gaggaggtgg 1920 30 gcgacgtece geeggegeae egteggegea eggeggeeeg acaceageag atggaegggg 1980 gaggeetgee eggaacegeg eageeggege gegaeetega aegeeaeegt ggeaeeeatg 2040 35 ctgtgcccga acagcgcgag cggacggtcg gcccagcgca ggatctccgg caccacctgg 2100 tecaceagge eegatatgga egggatgaae ggetegtgee ggeggteetg geggeeeggg 2160 tactgcaccg ccagcgcctc cacggtctcg tccagtccgc gtgccagggc ggcgaaggag 2220 40 gtcgcggcgc caccggcgtg cgggaagcag accagacgca gttccggatc ccgcaccggg 2280 eggtaaegge ggacecaeag accetegtee gggtgteegg eeggegaegg ggeteeegga 2340 45 acgggtggtg cggaaggggt gctcacggcg gatccagetc ctcgcggtcg gggggaccgc 2400 tgtcggggac ggcacgtcgg gtgcggacgt cgggtacggg cgtcggggcg tgacggggag 2460 ggacggggcg gtcggtcagt cggtgcgccg ggcctcctgc gcggccttct tcagcggttc 2520 50 2580 ccaccacgcg cggttctccg cgtaccagcg caccgtgtcc gccaggcccg tcgtgaagtc cgtacgcggg gcatagccca gctcgcccgt gatcttgccg atgtccagcg cgtaccgcag 2640 55 gtcgtgcccc ggccggtcgg cgacgtggcg caccgacgag gcgtcggcac cgcacagccc 2700 gagcagcege ttegteaget eceggttggt cageteegte eegecaeega tgtggtagae 2760 ctcgcccggg cgcccgcggg tcgccaccag gctgatcccg cggcagtggt cgtccacgtg 2820 60 cagccagtcc cggctgttgc cgccgtcgct gtacagcggc accgtcagac cgtccaacag 2880

	gttcgtggcg	aagagcggga	cgaccttctc	ggggtgctgg	tacgggccgt	agttgttgga	2940
5	gcaccgggtg	acgacgaccg	gcaggccgta	cgtccggtgg	taggccagcg	ccaggaggtc	3000
	cgacgccgcc	ttcgaggcgg	cgtacgggga	gttcggcgcc	agcggctgct	cctcgcgcca	3060
	cgacccctcg	gcgatcgagc	cgtacacctc	gtccgtggag	acgtggacga	accggccggc	3120
10	ccccgcctcc	accgcggcct	gcaagaggac	ttgcgtcccc	cgtacgttcg	tctcgacgaa	3180
	cgccgacgcg	teggegatgg	agcggtccac	gtgcgactcc	gccgcgaagt	ggaccacgac	3240
15	gtccgccccc	cgcacgaccc	gggacatcac	ctccgcgtcc	cggatgtcgg	cgtgcacgaa	3300
	ctccagcgac	ggatggtccg	cgaccgggtc	caggttggcg	aggttcccgg	cataggtcag	3360
	cttgtcgacc	accaccgtcc	gcgccccggc	caggtccgga	tacgccccgg	ccagcagttg	3420
20	tctgacgaag	tgcgagccga	tgaagcccgc	acctccggtg	accagcagcc	gcatgggagc	3480
	acagaccttt	cttccaggga	cgggaaacgg	ggaggcggac	ggggacggag	gcgagggcgg	3540
25	tggctatgcg	gccggtccgg	acatgagggt	ctccgccacg	tccatcaagt	accggccgta	3600
	gctggagctc	tcgagttcac	ggccgagctc	gtggcactgc	cgcgcgctga	tgtaccccat	3660
	ccgcagggcg	atctcctcga	cgcaggagat	ccgcacgccc	tgccgctgct	ccaggagctg	3720
30	gacgtactgc	cccgcttgca	gcagcgagct	gtgcgtgccc	atgtccagcc	aggcgaaccc	3780
	gcgccccagt	tccgtcatac	gggcgcggcc	ctgctccagg	tacaccttgt	tgacgtcggt	3840
35	gatctccage	tegeeeegeg	gcgacggtgt	cagccgccgg	gcgatgtcca	ccacgccgtt	3900
	gtcgtagaag	tacagccccg	tcaccgcgag	atgggagcgg	ggcttctccg	gcttctcctc	3960
	cagggacacc	agccggcctt	ccgcgtcgac	ctcgccgacg	ccgtagcgcc	gggggtcctt	4020
40	caccgggtag	ccgaacagct	cgcagccgtc	cageegee	gcggtggagg	ccagcacgga	4080
	ggagaacccc	ggaccgtgga	agacgttgtc	ccccaggatg	agggcgaccg	ggtcgtcccc	4140
45	gatgtgctcc	tcgccgatga	ggaacgcctc	ggcgatgccc	cggggctcct	cctgctcggc	4200
	gtagccgaca	ctgatcccga	tgcggctgcc	gtcgcccagc	agcgaacgga	acatctccaa	4260
	gtgcgtcttc	gacgtgatga	tctggatgtc	ccggatcccc	gccagcatga	gcaccgacag	4320
50	cgggtagtag	atcatgggct	tgtcgtagac	cggcagcaac	tgcttggaca	gtgccccggt	4380
	cagggggcgc	aggcgcgtgc	cgctgccgcc	cgccaggatg	atgcccttca	tgggccgccg	4440
55	gtccgccgtc	gtcttcgtca	t				4461

<sup>&</sup>lt;210> 7

<sup>&</sup>lt;211> 3375

<sup>&</sup>lt;212> DNA

<sup>60 &</sup>lt;213> Streptomyces eurythermus

				11/35			
	<400> 7 gtgagccccg	cacccgccac	cgaggacccg	gccgccgccg	ggcgccgcct	gcaactgacc	60
5	cgcgcagccc	agtggttcgc	gggaacccag	gacgacccgt	acgcgctcgt	cctgcgcgcc	120
•	gaggccaccg	acccggcccc	gtacgaggag	cggatccggg	cccacgggcc	gctcttccgc	180
	agcgacctgc	tcgacacctg	ggtcacggcg	agcagggccg	tcgccgacga	agtgatcacc	240
10	tcacccgcct	tcgacgggct	cacggccgac	gggcggcgcc	ccggcgcgcg	ggaactgccg	300
	ctgtccggca	ccgcgctcga	cgcggaccgc	gccacatgcg	cacggttcgg	ggccctcacc	360
15	gcctggggcg	ggccgctgct	gccggcgccg	cacgagcggg	cgctgcgcga	gtccgccgaa	420
15	cggcgggccc	acacactcct	cgacggggcg	gaggccgccc	tggccgccga	cggcaccgtc	480
	gacctcgtcg	acgcgtacgc	ccgcaggctc	cccgcgctgg	tcctccgcga	acagetegge	540
20	gtgccggagg	aggcggcgac	cgccttcgag	gacgcgctgg	ccggctgccg	ccgcaccctg	600
	gacggcgccc	tgtgcccgca	actcctcccg	gacgccgtgg	cgggggtgcg	cgcggaagcc	660
25	gcgctgaccg	ccgtgctggc	ctccgccctg	cgcgggactc	cggccggccg	ggcccccgac	720
	gccgtcgccg	ccgcccgcac	cctggccgtc	gcggccgccg	agcccgcagc	caccctcgtc	780
	ggcaacgccg	tacaggagct	gctggcgcgt	cccgcgcagt	gggcggagct	cgtacgcgac	840
30	ccgcgcctcg	cggccgccgc	ggtgaccgaa	acgctgcgtg	tegeceegee	cgtccgcctg	900
	gagcggcggg	tegecegega	ggacacggac	atcgccgggc	agegeeteee	cgccgggggg	960
35 .	agcgtcgtga	tcctcgtcgc	cgccgtcaac	cgcgcgcccg	tatccgcggg	aagcgacgcc	1020
	tccaccaccg	tcccgcacgc	cggcggccgg	ccccgtacct	ccgccccctc	cgtcccctca	1080
	gcccccttcg	acctcacacg	gcccgtggcc	gegeeeggge	cgttcgggct	ccccggcgac	1140
40	ctgcacttcc	gcctcggcgg	gcccctggtc	ggaacggtcg	ccgaagccgc	gctcggtgcg	1200
	ctggccgcac	ggctccccgg	tctgcgcgcc	gccgggccgg	ccgtgcggcg	ccgccgctca	1260
45	ccggtgctgc	acggacacgc	ccgcctcccc	gtcgccgtcg	cccggacggc	ccgtgacctg	1320
	cccgccaccg	caccgcggaa	ctgaggaggg	agtgccccga	tgcgtatcct	gctgacgtcg	1380
	ttcgcgcaca	acacgcacta	ctacaacctg	gtcccctcg	gctgggcgct	gcgcgccgcc	1440
50	gggcacgacg	tacgggtcgc	cagccagccc	tcgctgaccg	gcaccatcac	cggctccggg	1500
	ctgaccgccg	tccccgtggg	cgacgacacg	gccatcgtcg	agctgatcac	cgagatcggc	1560
55	gacgacctcg	tcctctacca	gcagggcatg	gacttcgtgg	acacccgcga	cgagccgctg	1620
	tcctgggaac	acgccctcgg	acagcagacg	atcatgtcgg	ccatgtgctt	ctcgccgctg	1680
	aacggcgaca	gcaccatcga	cgacatggtg	gcgctggccc	gttcctggaa	accggacctc	1740
60	gtcctgtggg	agcccttcac	ctacgcggga	cccgtcgccg	cgcacgcctg	cggcgccgcc	1800

12/35

				12/33			
	cacgcccggc	tgctgtgggg	tcccgacgtg	gtcctcaacg	cacggcggca	gttcacccgg	1860
	ctgctcgccg	agcgccccgt	cgaacagcgc	gaggacccgg	tcggcgaatg	gctcacgtgg	1920
5	acgctggagc	gccacggcct	cgccgccgac	gcggacacga	tcgaggaact	gttcgccggg	1980
	cagtggacga	tcgaccccag	cgccgggagc	ctgcggctgc	cggtcgacgg	cgaggtcgtg	2040
10	cccatgcgct	tcgtgccgta	caacggcgcc	teggtegtee	ccgcctggct	ctccgagccg	2100
	cctgcccggc	cccgggtctg	cgtcaccctc	ggcgtctcca	cccgggagac	ctacggcacg	2160
	gacggcgtcc	cgttccacga	actgctggcc	ggactggccg	acgtggacgc	cgagatcgtc	2220
15	gccaccctcg	acgcggggca	gctcccggac	gccgccggtc	tgcccggcaa	tgtgcgcgtc	2280.
	gtcgacttcg	tgccgctgga	cgccctgctg	ccgagctgcg	ccgcgatcgt	ccaccacgga	2340
20	ggcgcgggaa	cctgtttcac	ggccaccgtg	cacggcgtcc	cgcagatcgt	cgtggcctcc	2400
20	ctctgggacg	cgccgctgaa	ggcgcaccaa	ctcgccgagg	cgggcgccgg	gatcgccctg	2460
	gaccccgggg	aactgggcgt	ggacaccctg	cgcggcgccg	tcgtgcgggt	gctggagagc	2520
25	cgcgagatgg	ccgtggcggc	gcgtcgcctc <sub>.</sub>	gccgacgaga	tgctcgccgc	ccccaccccg	2580
	gccgcgctcg	tecceegect	cgaacgcctc	accgccgcgc	accgccgcgc	ctgatcccgc	2640
30	caaggagccc	ccatgaacct	cgaatacagc	ggcgacatcg	cccggttgta	cgacctggtc	2700
	caccagggaa	agggcaagga	ctaccgggcg	gaggccgagg	agctggccgc	gcttgtcacc	2760
	cagegeegee	ccggggcccg	ctccctcctc	gacgtggcct	gcggaacggg	gatgcacctg	2820
35	cggcacctcg	gcgacctctt	cgaggaggtg	gccggggtgg	agatgtcccc	cgacatgctg	2880
	gccatcgcgc	agcggcgcaa	cccggaggcc	ggcatccacc	ggggggacat	gcgggacttc	2940
40	gccctcggcc	gccgcttcga	cgccgtgatc	tgcatgttca	gttccatcgg	gcacatgcgc	3000
	gaccagcggg	aactggacgc	ggcgatcggc	cggttcgccg	cgcacctgcc	gtccggcggg	3060
	gtcgtgatcg	tcgatccctg	gtggttcccg	gagacgttca	caccggggta	cgtcggcgcg	3120
45	agcctcgtcg	aggccgaggg	ccgcaccatc	gcgcgcttct	cccactccgc	gctcgaggac	3180
	ggcgcgaccc	ggatcgatgt	ggactacctc	gtcggcgtgc	cgggggaggg	ggtgcggcac	3240
50	ttgaaggaga	cccatcggat	cacgcttttc	gggcgtgcgc	agtacgaggc	ggccttcacc	3300
	gcggcgggga	tgtccgtcga	gtacctcccg	cacgccgcca	ccgaccgcgg	actcttcgtc	3360
	ggcgtccagg	cctga					3375
55	<210> 8 <211> 295 <212> PRT						

60 <400> 8

<sup>&</sup>lt;213> Streptomyces eurythermus

c	Met 1	Lys	Gly	/ Ile	: Ile 5	. Leu	Ala	Gly	Gly	Ser 10	Gly	Thr	Arg	Leu	Arg 15	Pro
5	Lev	ı Thr	: Gly	Ala 20	Leu	Ser	Lys	Gln	Leu 25	Leu	Pro	Val	Tyr	Asp 30	Lys	Pro
10	Met	: Ile	Туг 35	Tyr	Pro	Leu	Ser	Val 40	Leu	Met	Leu	Ala	Gly 45	Ile	Arg	Asp
15	Ile	Gln 50	Ile	Ile	Thr	Ser	Lys 55	Thr	His	Leu	Glu	Met 60	Phe	Arg	Ser	Leu
20	Leu 65	Gly	Asp	Gly	Ser	Arg 70	Ile	Gly	Ile	Ser	Val 75	Gly	Tyr	Ala	Glu	Gln 80
25	Glu	Glu	Pro	Arg	Gly 85	Ile	Ala	Glu	Ala	Phe 90	Leu	Ile	Gly	Glu	Glu 95	His
23	Ile	Gly	Asp	Asp 100	Pro	Val	Ala	Leu	Ile 105	Leu	Gly	Asp	Asn	Val 110	Phe	His
30	Gly	Pro	Gly 115	Phe	Ser	Ser	Val	Leu 120	Ala	Ser	Thr	Ala	Ala 125	Arg	Leu	Asp
35	Gly	Cys 130	Glu	Leu	Phe	Gly	Tyr 135	Pro	Val	Lys	Asp	Pro 140	Arg	Arg	Tyr	Gly
40	Val 145	Gly	Glu	Val	Asp	Ala 150	Glu	Gly	Arg	Leu	Val 155	Ser	Leu	Glu	Glu	Lys 160
45	Pro	Glu	Lys	Pro	Arg 165	Ser	His	Leu		Val 170		Gly	Leu		Phe 175	
45	Asp	Asn	Gly	Val 180	Val	Asp	Ile	Ala	Arg 185	Arg	Leu	Thr	Pro	Ser 190	Pro	Arg
50	Gly	Glu	Leu 195	Glu	Ile	Thr	Asp	Val 200	Asn	Lys	Val	Tyr	Leu 205	Glu	Gln	Gly
55	Arg	Ala 210	Arg	Met	Thr	Glu	Leu 215	Gly	Arg	Gly	Phe	Ala 220	Trp	Leu	Asp	Met
50	Gly 225	Thr	His	Ser	Ser	Leu 230	Leu	Gln	Ala	Gly	Gln 235	Tyr	Val	Gln	Leu	Leu 240

14/35

Glu Gln Arg Gln Gly Val Arg Ile Ser Cys Val Glu Glu Ile Ala Leu 245 250 255

- 5 Arg Met Gly Tyr Ile Ser Ala Arg Gln Cys His Glu Leu Gly Arg Glu 260 265 270
- Leu Glu Ser Ser Tyr Gly Arg Tyr Leu Met Asp Val Ala Glu Thr 275 280 285
- Leu Met Ser Gly Pro Ala Ala 290 295
- <210> 9
- <211> 332 <212> PRT

30

- 20 <213> Streptomyces eurythermus
  - <400> 9
- - Val Arg Gln Leu Leu Ala Gly Ala Tyr Pro Asp Leu Ala Gly Ala Arg 20 25 30
    - Thr Val Val Asp Lys Leu Thr Tyr Ala Gly Asn Leu Ala Asn Leu 35 40
- Asp Pro Val Ala Asp His Pro Ser Leu Glu Phe Val His Ala Asp Ile
  50 55 60
- 40 Arg Asp Ala Glu Val Met Ser Arg Val Val Arg Gly Ala Asp Val Val 65 70 75 80
- Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Ala Asp Ala 45 85 90 95
- Ser Ala Phe Val Glu Thr Asn Val Arg Gly Thr Gln Val Leu Gln  $100 \\ 105 \\ 110 \\ 105$ 
  - Ala Ala Val Glu Ala Gly Ala Gly Arg Phe Val His Val Ser Thr Asp 115 120 125
- Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Arg Glu Glu Gln Pro
  130 135 140
- 60 Leu Ala Pro Asn Ser Pro Tyr Ala Ala Ser Lys Ala Ala Ser Asp Leu 145 150 155 160

5	Leu	Ala	Leu	Ala	Tyr 165	His	Arg	Thr	Tyr	Gly 170	Leu	Pro	Val	Val	Val 175	Thr
10	Arg	Суѕ	Ser	Asn 180	Asn	Tyr	Gly	Pro	Tyr 185	Gln	His	Pro	Glu	Lys 190	Val	Val
10	Pro	Leu	Phe 195	Ala	Thr	Asn	Leu	Leu 200	Asp	Gly	Leu	Thr	Val 205	Pro	Leu	Tyr
15	Ser	Asp 210	Gly	Gly	Asn	Ser	Arg 215	Asp	Trp	Leu	His	Val 220	Asp	Asp	His	Cys
20	Arg 225	Gly	Ile	Ser	Leu	Val 230	Ala	Thr	Arg	Gly	Arg 235	Pro	Gly	Glu	Val	Tyr 240
25	His	Ile	Gly	Gly	Gly 245	Thr	Glu	Leu	Thr	Asn 250	Arg	Glu	Leu	Thr	Lys 255	Arg
	Leu	Leu	Gly	Leu 260	Cys	Gly	Ala	Asp	Ala 265	Ser	Ser	Val	Arg	His 270	Val	Ala
30	Asp	Arg	Pro 275	Gly	His	Asp	Leu	Arg 280	Tyr	Ala	Leu	Asp	Ile 285	Gly	Lys	Ile
35	Thr	Gly 290	Glu	Leu	Gly	Tyr	Ala 295	Pro	Arg	Thr	Asp	Phe 300	Thr	Thr	Gly	Leu
40	Ala . 305	Asp	Thr	Val	Arg	Trp 310	Tyr	Ala	Glu	Asn	Arg 315	Ala	Trp	Trp	Glu	Pro 320
45	Leu :	Lys	Lys	Ala	Ala 325	Gln	Glu	Ala	Arg	Arg 330	Thr	Asp				
50	<210: <211: <212: <213:	> 7 > P	0 87 RT trep	tomy	ces.	eury	<i>r</i> ther	mus								
	<400	> 1	0													
55	Val s	Ser	Thr	Pro	Ser 5	Ala	Pro	Pro	Val	Pro 10	Gly	Ala	Pro	Ser	Pro 15	Ala
60	Gly F	lis		Asp 20	Glu	Gly	Leu	Trp	Val 25	Arg	Arg	Tyr	Arg	Pro 30	Val	Arg

GB2004/005001

		wo	2005/	05426	5											PCT/C
	Asp	Pro	Glu 35	Leu	Arg	Leu	Val	Cys 40	Phe	16/ Pro		Ala	Gly 45	Gly	Ala	Ala
5	Thr	Ser 50	Phe	Ala	Ala	Leu	Ala 55	Arg	Gly	Leu	Asp	Glu 60	Thr	Val	Glu	Ala
10	Leu 65	Ala	Val	Gln	Tyr	Pro 70	Gly	Arg	Gln	Asp	Arg 75	Arg	His	Glu	Pro	Phe 80
15	Ile	Pro	Ser	Ile	Ser 85	Gly	Leu	Val	Asp	Gln 90	Val	Val	Pro	Glu	Ile 95	Leu
20	Arg	Trp	Ala	Asp 100	Arg	Pro	Leu	Ala	Leu 105	Phe	Gly	His	Ser	Met 110	Gly	Ala
	Thr	Val	Ala 115	Phe	Glu	Val	Ala	Arg 120	Arg	Leu	Arg	Gly	Ser 125	Gly	Gln	Ala
25	Ser	Pro 130	Val	His	Leu	Leu	Val 135	Ser	Gly	Arg	Arg	Ala 140	Pro	Thr	Val	Arg
30	Arg 145	Arg	Asp	Val	Ala	His 150	Leu	Leu	Asp	Asp	Asp 155	Ala	Leu	Ile	Ala	Glu 160
35	Ile	Ala	Thr	Leu	Gln 165	Gly	Thr	Glu	Asp	Ala 170	Val	Leu	Gln	Asp	Glu 175	Glu

Leu Leu Arg Leu Ala Leu Pro Ala Ile Arg Asn Asp Tyr Arg Ala Ala

Gly Thr Tyr Ala Tyr Val Pro Gly Gly Ala Leu Asp Cys Pro Val Thr

Val Leu Thr Gly Asp Arg Asp Pro Asp Val Pro Leu Glu Glu Ala Arg

Ala Trp Arg Glu Leu Thr Thr Gly Pro Phe Ala Leu His Thr Phe Ala

Gly Gly His Phe Tyr Leu Asn Asp Arg Met Asp Glu Val Cys Arg Thr

Ile Gly Asp Ala Leu Ala Gly Thr Ala Thr Ala Asp Thr Ala Thr Gly

Thr Val Pro Pro Arg Thr Ala Ala Asp Thr Ser Thr Gly Pro Val Pro

275 280 285

5	Pro	Arg 290	Thr	Ala	Ala	Asp	Thr 295	Ala	Arg	Glu	Pro	Val 300	Pro	Pro	Arg	Ser
10	Ala 305	Pro	Ala	Pro	His	Gly 310	Ala	Ala	Arg	Arg	Arg 315	Ala	Asp	Ala	Val	Arg 320
	Pro	Gly	Asp	Pro	Val 325	Asp	Thr	Ala	Arg	Arg 330	Val	Leu	Val	Ser	Ala 335	Arg
15	Thr	Ala	Asp	Ser 340	Ala	Val	Thr	Pro	Phe 345	Asp	Gly	Ile	Ser	Gly 350	Trp	Leu
20	Ala	Glu	Arg 355	Leu	Arg	Ala	Gly	Arg 360	Phe	Asp	Val	Ser	Arg 365	Val	Pro	Phe
25	Ala	Glu 370	Leu	Arg	Gly	Trp	Ser 375	Phe	His	Pro	Gly	Thr 380	Gly	Asn	Leu	His
30	His 385	Ala	Ser	Gly	Arg	Phe 390	Phe	Ser	Val	Glu	Gly 395	Leu	His	Val	Arg	Thr 400
	Asp	Arg	Leu	Pro	Glu 405	Arg	Gly	Trp	Thr	Gln 410	Pro	Ile	Ile	Val	Gln 415	Pro
35	Glu	Val	Gly	Leu 420	Leu	Gly	Ile	Val	Ala 425	Arg	Glu	Ile	Asp	Gly 430	Val	Leu
40	His	Phe	Leu 435	Met	Gln	Ala	Lys	Met 440	Glu	Pro	Gly	Asn	Val 445	Asn	Val	Leu
45	Gln	Val 450	Ser	Pro	Thr	Val	Gln 455	Ala	Thr	Arg	Ser	Asn 460	Phe	Thr	Gly	Val
50	His 465	Arg	Gly	Arg	Asp	Ile 470	Arg	Tyr	Leu	Asp	Leu 475	Phe	Met	Gly	Pro	Arg 480
	Arg	Ala	Arg	Val	Leu 485	Val	Asp	Ser	Ile	Gln 490	Ser	Glu	Gln	Ala	Asp 495	Trp
55	Phe	Leu	Ala	Lys 500	Arg	Asn	Arg	Asn	Met 505	Ile	Val	Glu	Leu	Ala 510	Ala	Asp
60	Asp	Asp	Leu 515	Asp	Ile	Gly	Glu	Asp 520	Phe	Arg	Trp	Leu	Thr 525	Leu	Gly	Gln

Leu Arg Arg Leu Leu Met Leu Asp Asn Val Val Asn Met Asp Ala Arg Ser Ile Leu Ala Cys Leu Pro Thr Ala Asp Ala Asp Ala Ser Ala Pro Ser Pro Val Leu Arg Ser Phe Phe Gly Ser Pro Gly Ala Ala Arg His Thr Thr Ala Glu Val Leu Thr Trp Phe Thr Gly Val Arg Ala Leu Arg Glu Leu Val Gln Asn Arg Val Pro Leu Asp Thr Val Thr Ala Asp Gly Trp Tyr Arg Thr Pro His Glu Ile Ala His Glu Ser Gly Arg His Phe Arg Val Met Ala Ala Glu Val Ser Ala Ser Ser Arg Glu Val Thr Ser Trp Thr Gln Pro Leu Ile Glu Pro Arg Leu Pro Gly Leu Met Ala Leu Leu Val Lys Ser Val Asp Gly Val Leu His Ala Leu Val Arg Ala Arg Val Asp Val Gly His Leu Asn Val Ala Glu Leu Ala Pro Thr Val Gln Cys Arg Pro Gln Glu His Thr Gly Pro Arg Gly Leu Pro Gly Pro Pro Tyr Leu Glu Asp Val Leu Ser Ala Pro Pro Gln Asp Val Arg Tyr Asp Ala Val Gln Ser Glu Glu Gly Gly Arg Phe Phe His Ala Gln Asn Arg Tyr Val Ile Val Glu Val Pro His Asp Phe Pro Glu Asp Ala Pro Asp Asp Phe Ala Trp Leu Ser Leu Gly Gln Leu Thr Gly Leu Leu Ala His 

	Gly Asn Tyr Leu Asn Ile Glu Leu Arg Thr Leu Val Ala Cys Ala His															
	Gly	Asn 770	Tyr	Leu	Asn	Ile	Glu 775	Leu	Arg	Thr	Leu	Val 780	Ala	Cys	Ala	His
5	Thr 785	Leu	Tyr													
10	<210 <213 <213 <213	l> : 2> :	11 333 PRT Strep	otomy	ces/	eury	/ther	mus								
15	<400	)> :	11													
	Met 1	Val	Asn	Asp	Pro 5	Met	Pro	Arg	Gly	Ser 10	Gly	Ser	Gly	Ser	Val 15	Val
20	Val	Leu	Gly	Gly 20	Ala	Gly	Tyr	Val	Gly 25	Arg	His	Val	Cys	Ala 30	Ala	Phe
25	Ala	Ala	Arg 35	Gly	Arg	Asp	Val	Val 40	Val	Val	Gly	Arg	Arg 45	Pro	Pro	Glu
30	Glu	Pro 50	Met	Pro	Tyr	Arg	Cys 55	Val	Thr	Leu	Asp	Leu 60	Ala	Gly	Thr	Asp
35	Pro 65	Ala	Ala	Leu	Ala	Ala 70	Ala	Leu	Asp	Ala	Glu 75	Arg	Pro	Asp	Thr	Ile 80
	Val	Asn	Ser	Val	Gly 85	Ser	Ile	Trp	Gly	Arg 90	Thr	Asp	Glu	Gln	Met 95	Trp
40	Ser	Ala	Thr	Ala 100	Val	Pro	Thr	Leu	Arg 105	Leu	Leu	Glu	Ala	Leu 110	Ala	Leu
45	Met	Ser	Ala 115	Arg	Pro	Arg	Leu	Val 120	His	Leu	Gly	Ser	Val 125	Leu	Glu	Tyr
50	Gly	Pro 130	Val	Thr	Pro	Gly	Gly 135	Ser	Val	Gly	Ala	Asp 140	Ala	Val	Pro	Arg
55	Pro 145	Asp	Thr	Ala	Tyr	Gly 150	Arg	Ser	Lys	Leu	Ala 155	Ala	Ser	Glu	Ala	Val 160
	Leu	Arg	Gly	Thr	Ser 165	Gly	Gly	Trp	Val	Asp 170	Gly	Val	Val	Leu	Arg 175	Val
60	Ser	Asn	Val	Ser	Gly	Pro	Gly	Thr	Pro	Arg	Ile	Ser	Leu	Leu	Gly	Gln

20/35

190 Val Ala Glu Arg Leu Leu Ala Ala Gly Thr Gly Ala Glu Ala Val 5 Val Glu Leu Ser Arg Leu Arg Ala His Arg Asp Tyr Val Asp Val Arg 215 10 Asp Val Ala Asp Ala Val Val Ala Ala Ala Arg Ala Pro Ala Val Pro 225 15 Val Ala Val Gly Ile Gly Arg Gly Glu Ala Val Ala Val Arg Asp Leu 20 Val Gly Leu Phe Ile Glu Ala Ser Gly Ile Pro Ala Arg Val Val Glu Arg Pro Ala Pro Gly Arg Ala Pro Gly His Arg Glu Asp Trp Leu Arg 25 Val Asp Thr Gly Ala Ala Arg Ala Leu Leu Gly Trp Ala Pro Arg Arg 30 Ser Leu Arg Glu Ser Val Arg Asp Cys Trp His Asp Leu Val Arg Ala 315 35 His Arg Leu Pro Thr Thr Pro Ser Lys His Ser Gly Gly 10 <210> 12 <211> 373 <212> PRT <213> Streptomyces eurythermus 15 <400> 12 Val Thr Thr Tyr Val Trp Asp Tyr Leu Ala Glu Tyr Gln Asn Glu Arg 5 50 Ala Asp Leu Leu Asp Ala Val Glu Thr Val Phe Ala Ser Gly Gln Leu 20 25 30 **i**5 Val Leu Gly Pro Ser Val Asp Gly Phe Glu Lys Glu Phe Ala Asp Tyr 35 40 His Gly Leu Arg His Cys Gly Gly Val Asp Asn Gly Thr Asn Ala Val **i**0 55 60

	Lys 65	Leu	Gly	Leu	Gln	Ala 70	Leu	Gly	Val	Gly	Pro 75	Gly	Asp	Glu	Val	Val 80
5	Thr	Val	Ser	Asn	Thr 85	Ala	Ala	Pro	Thr	Val 90	Val	Ala	Ile	Asp	Gly 95	Thr
10	Gly	Ala	Thr	Pro 100	Val	Phe	Val	Asp	Val 105	Arg	Ala	Glu	Asp	His 110	Leu	Met
15	Asp	Thr	Asp 115	Gln	Val	Ala	Asp	Val 120	Ile	Thr	Pro	Arg	Thr 125	Lys	Ala	Leu
20	Leu	Pro 130	Val	His	Leu	Tyr	Gly 135	Gln	Cys	Val	Asp	Met 140	Ala	Pro	Leu	Arg
	Ala 145	Leu	Ala	Glu	Gln	His 150	Gly	Leu	Val	Val	Leu 155	Glu	Asp	Cys	Ala	Gln 160
25	Ala	His	Gly	Ala	Arg 165	His	His	Gly	Glu	Leu 170	Ala	Gly	Thr	Leu	Gly 175	Asp
30	Ala	Ala	Ala	Phe 180	Ser	Phe	Tyr	Pro	Thr 185	Lys	Val	Leu	Gly	Ala 190	Tyr	Gly
35	Asp	Gly	Gly 195	Ala	Val	Leu	Thr	Asp 200	Asp	Ala	Asp	Val	Asp 205	Arg	Ala	Leu
40	Arg	Arg 210	Leu	Arg	Tyr	Tyr	Gly 215	Met	Glu	Asp	Val	Tyr 220	Tyr	Val	Val	Gln
	Thr 225		Gly	His		Ser 230		Leu	Asp		Val 235		Ala	Glu	Ile	Leu 240
45	Arg	Arg	Lys	Leu	Thr 245	Arg	Leu	Asp	Arg	Tyr 250	Ile	Glu	Gly	Arg	Arg 255	Ala
50	Val	Ala	Arg	Arg 260	Tyr	Ala	Glu	Gly	Leu 265	Ala	Asn	Leu	Thr	Gly 270	Pro	Gly
55	Gly	Leu	Val 275	Leu	Pro	Ser	Val	Thr 280	Glu	Gly	Asn	Asp	His 285	Val	Tyr	Tyr
60	Val	Tyr 290	Val	Val	Arg	His	Pro 295	Arg	Arg	Asp	Asp	Ile 300	Ile	Glu	Ala	Leu

	22/35 Lys Ser Tyr Gly Ile Ser Leu Asn Ile Ser Tyr Pro Trp Pro Val H															
	Lys 305	Ser	Tyr	Gly	Ile	Ser 310	Leu	Asn	Ile			Pro	Trp	Pro	Val	His 320
5	Thr	Met	Thr	Gly	Phe 325	Ala	His	Leu	Gly	Tyr 330	Ala	Lys	Gly	Ser	Leu 335	Pro
10	Val	Thr	Glu	Arg 340	Leu	Ala	Asp	Glu	Ile 345	Phe	Ser	Leu	Pro	Met 350	Tyr	Pro
15	Gly	Leu	Ala 355	Pro	Asp	Val	Gln	Asp 360	Lys	Val	Ile	Ala	Ala 365	Leu	His	Glu
	Val	Leu 370	Ala	Thr	Leu											
20	<210 <210 <210	1> 4	13 447 PRT						•							
25	<21		Strep	otomy	yces	eury	ythei	cmus								
23	<40	0> :	13									•				
30	Val 1	Ser	Pro	Ala	Pro 5	Ala	Thr	Glu	Asp	Pro 10	Ala	Ala	Ala	Gly	Arg 15	Arg
	Leu	Gln	Leu	Thr 20	Arg	Ala	Ala	Gln	Trp 25	Phe	Ala	Gly	Thr	Gln 30	Asp	Asp
35	Pro	Tyr	Ala 35	Leu	Val	Leu	Arg	Ala 40	Glu	Ala	Thr	Asp	Pro 45	Ala	Pro	Tyr
40	Glu	Glu 50	Arg	Ile	Arg	Ala	His 55	Gly	Pro	Leu	Phe	Arg 60	Ser	Asp	Leu	Leu
45	Asp 65	Thr	Trp	Val	Thr	Ala 70	Ser	Arg	Ala	Val	Ala 75	Asp	Glu	Val	Ile	Thr 80
50	Ser	Pro	Ala	Phe	Asp 85	Gly	Leu	Thr	Ala	Asp 90	Gly	Arg	Arg	Pro	Gly 95	Ala
	Arg	Glu	Leu	Pro 100	Leu	Ser	Gly	Thr	Ala 105	Leu	Asp	Ala	Asp	Arg 110	Ala	Thr
55	Cys	Ala	Arg 115	Phe	Gly	Ala	Leu	Thr 120	Ala	Trp	Gly	Gly	Pro 125	Leu	Leu	Pro
60	Ala	Pro 130	His	Glu	Arg	Ala	Leu 135	Arg	Glu	Ser	Ala	Glu 140	Arg	Arg	Ala	His

WO 2005/054265 PCT/GB2004/005001 23/35

5	Thr 145	Leu	Leu	Asp	Gly	Ala 150	Glu	Ala	Ala	Leu	Ala 155	Ala	Asp	Gly	Thr	Val 160
	Asp	Leu	Val	Asp	Ala 165	Tyr	Ala	Arg	Arg	Leu 170	Pro	Ala	Leu	Val	Leu 175	Arg
10	Glu	Gln	Leu	Gly 180	Val	Pro	Glu	Glu	Ala 185	Ala	Thr	Ala	Phe	Glu 190	Asp	Ala
15	Leu	Ala	Gly 195	Cys	Arg	Arg	Thr	Leu 200	Asp	Gly	Ala	Leu	Cys 205	Pro	Gln	Leu
20	Leu	Pro 210	Asp	Ala	Val	Ala	Gly 215	Val	Arg	Ala	Glu	Ala 220	Ala	Leu	Thr	Ala
25	Val 225	Leu	Ala	Ser	Ala	Leu 230	Arg	Gly	Thr	Pro	Ala 235	Gly	Arg	Ala	Pro	Asp 240
	Ala	Val	Ala	Ala	Ala 245	Arg	Thr	Leu	Ala	Val 250	Ala	Ala	Ala	Glu	Pro 255	Ala
30	Ala	Thr	Leu	Val 260	Gly	Asn	Ala	Val	Gln 265	Glu	Leu	Leu	Ala	Arg 270	Pro	Ala
35	Gln	Trp	Ala 275	Glu	Leu	Val	Arg	Asp 280	Pro	Arg	Leu	Ala	Ala 285	Ala	Ala	Val
40	Thr	Glu 290	Thr	Leu	Arg	Val	Ala 295	Pro	Pro	Val	Arg	Leu 300	Glu	Arg	Arg	Val
45	Ala 305		Glu	Asp		Asp 310		Ala	Gly		Arg 315		Pro	Ala	Gly	Gly 320
	Ser	Val	Val	Ile	Leu 325	Val	Ala	Ala	Val	Asn 330	Arg	Ala	Pro	Val	Ser 335	Ala
50	Gly	Ser	Asp	Ala 340	Ser	Thr	Thr	Val	Pro 345	His	Ala	Gly	Gly	Arg 350	Pro	Arg
55	Thr	Ser	Ala 355	Pro	Ser	Val	Pro	Ser 360	Ala	Pro	Phe	Asp	Leu 365	Thr	Arg	Pro
60	Val	Ala 370	Ala	Pro	Gly	Pro	Phe 375	Gly	Leu	Pro	Gly	Asp 380	Leu	His	Phe	Arg

	Leu 385	Gly	Gly	Pro	Leu	Val 390	Gly	Thr	Val	Ala	Glu 395	Ala	Ala	Leu	Gly	Ala 400
5	Leu	Ala	Ala	Arg	Leu 405	Pro	Gly	Leu	Arg	Ala 410	Ala	Gly	Pro	Ala	Val 415	Arg
10	Arg	Arg	Arg	Ser 420	Pro	Val	Leu	His	Gly 425	His	Ala	Arg	Leu	Pro 430	Val	Ala
15	Val	Ala	Arg 435	Thr	Ala	Arg	Asp	Leu 440	Pro	Ala	Thr	Ala	Pro 445	Arg	Asn	
20	<210 <211 <212 <213	L> 4 2> I	L4 424 PRT Strep	otomy	/ces	eury	/thei	cmus								
•	<400	)> :	L 4													
25	Met 1	Arg	Ile	Leu	Leu 5	Thr	Ser	Phe	Ala	His 10	Asn	Thr	His	Tyr	Tyr 15	Asn
30	Leu	Val	Pro	Leu 20	Gly	Trp	Ala	Leu	Arg 25	Ala	Ala	Gly	His	Asp 30	Val	Arg
35	Val	Ala	Ser 35	Gln	Pro	Ser	Leu	Thr 40	Gly	Thr	Ile	Thr	Gly 45	Ser	Gly	Leu
	Thr	Ala 50	Val	Pro	Val	Gly	Asp 55	Asp	Thr	Ala	Ile	Val 60	Glu	Leu	Ile	Thr
40	Glu 65	Ile	Gly	Asp	Asp	Leu 70	Val	Leu	Tyr	Gln	Gln 75	Gly	Met	Asp	Phe	Val 80
45	Asp	Thr	Arg	Asp	Glu 85	Pro	Leu	Ser	Trp	Glu 90	His	Ala	Leu	Gly	Gln 95	Gln
50	Thr	Ile	Met	Ser 100	Ala	Met	Cys	Phe	Ser 105	Pro	Leu	Asn	Gly	Asp 110	Ser	Thr
55	Ile	Asp	Asp 115	Met	Val	Ala	Leu	Ala 120	Arg	Ser	Trp	Lys	Pro 125	Asp	Leu	Val
	Leu	Trp 130	Glu	Pro	Phe	Thr	Tyr 135	Ala	Gly	Pro	Val	Ala 140	Ala	His	Ala	Cys
60	Gly	Ala	Ala	His	Ala	Arg	Leu	Leu	Trp	Gly	Pro	Asp	Val	Val	Leu	Asn

		wo	2005/0	05426	5											PCT/
•	145					150				25/	35 155					160
5	Ala	Arg	Arg	Gln	Phe 165	Thr	Arg	Leu	Leu	Ala 170	Glu	Arg	Pro	Val	Glu 175	Gln
10	Arg	Glu	Asp	Pro 180	Val	Gly	Glu	Trp	Leu 185	Thr	Trp	Thr	Leu	Glu 190	Arg	His
	Gly	Leu	Ala 195	Ala	Asp	Ala	Asp	Thr 200	Ile	Glu	Glu	Leu	Phe 205	Ala	Gly	Gln
15	Trp	Thr 210	Ile	Asp	Pro	Ser	Ala 215	Gly	Ser	Leu	Arg	Leu 220	Pro	Val	Asp	Gly
20	Glu 225	Val	Val	Pro	Met	Arg 230	Phe	Val	Pro	Tyr	Asn 235	Gly	Ala	Ser	Val	Val 240
25	Pro	Ala	Trp	Leu	Ser 245	Glu	Pro	Pro	Ala	Arg 250	Pro	Arg	Val	Cys	Val 255	Thr
30	Leu	Gly	Val	Ser 260	Thr	Arg	Glu	Thr	Tyr 265	Gly	Thr	Asp	Gly	Val 270	Pro	Phe
	His	Glu	Leu 275	Leu	Ala	Gly	Leu	Ala 280	Asp	Val	Asp	Ala	Glu 285	Ile	Val	Ala
35	Thr	Leu 290	Asp	Ala	Gly	Gln	Leu 295	Pro	Asp	Ala	Ala	Gly 300	Leu	Pro	Gly	Asn
40	Val 305	Arg	Val	Val	Asp	Phe 310	Val	Pro	Leu	Asp	Ala 315	Leu	Leu	Pro	Ser	Cys 320
45	Ala	Ala	Ile	Val	His 325	His	Gly	Gly	Ala	Gly 330	Thr	Cys	Phe	Thr	Ala 335	Thr
50	Val	His	Gly	Val 340	Pro	Gln	Ile	Val	Val 345	Ala	Ser	Leu	Trp	Asp 350	Ala	Pro
	Leu	Lys	Ala 355	His	Gln	Leu	Ala	Glu 360	Ala	Gly	Ala	Gly	Ile 365	Ala	Leu	Asp
55	Pro	Gly 370	Glu	Leu	Gly	Val	Asp 375	Thr	Leu	Arg	Gly	Ala 380	Val	Val	Arg	Val
50	Leu 385	Glu	Ser	Arg	Glu	Met 390	Ala	Val	Ala	Ala	Arg 395	Arg	Leu	Ala	Asp	Glu 400

5	Met	Leu	Ala	Ala	Pro 405	Thr	Pro	Ala	Ala	Leu 410	Val	Pro	Arg	Leu	Glu 415	Arg
	Leu	Thr	Ala	Ala 420	His	Arg	Arg	Ala								
10	<21 <21 <21	1>	15 240 PRT													
15	<21		Stre	ptomy	yces	eury	ythe	cmus								
	<40		15	<b>01</b>	m	0	<b>61</b>				_	_		_		
20	Met 1	AST	Leu	GIU	Tyr 5	Ser	СТĀ	Asp	lle	Ala 10	Arg	Leu	Tyr	Asp	Leu 15	Val
26	His	Gln	Gly	Lys 20	Gly	Lys	Asp	Tyr	Arg 25	Ala	Glu	Ala	Glu	Glu 30	Leu	Ala
25	Ala	Leu	Val 35	Thr	Gln <sup>'</sup>	Arg	Arg	Pro 40	Gly	Ala	Arg	Ser	Leu 45	Leu	Asp	Val
30	Ala	Cys 50	Gly	Thr	Gly	Met	His 55	Leu	Arg	His	Leu	Gly 60	Asp	Leu	Phe	Glu
35	Glu 65	Val	Ala	Gly	Val	Glu 70	Met	Ser	Pro	Asp	Met 75	Leu	Ala	Ile	Ala	Gln 80
40	Arg	Arg	Asn	Pro	Glu 85	Ala	Gly	Ile	His	Arg 90	Gly	Asp	Met	Arg	Asp 95	Phe
	Ala	Leu	Gly	Arg 100	Arg	Phe	Asp	Ala	Val 105	Ile	Cys	Met	Phe	Ser 110	Ser	Ile
45	Gly	His	Met 115	Arg	Asp	Gln	Arg	Glu 120	Leu	Asp	Ala	Ala	Ile 125	Gly	Arg	Phe
50	Ala	Ala 130	His	Leu	Pro	Ser	Gly 135	Gly	Val	Val	Ile	Val 140	Asp	Pro	Trp	Trp
55	Phe 145	Pro	Glu	Thr	Phe	Thr 150	Pro	Gly	Tyr	Val	Gly 155	Ala	Ser	Leu	Val	Glu 160
50	Ala	Glu	Gly	Arg	Thr 165	Ile	Ala	Arg	Phe	Ser 170	His	Ser	Ala	Leu	Glu 175	Asp

	Gly Ala	Thr	Arg 180	Ile	Asp	Val	Asp	Tyr 185	Leu	Val	Gly	Val	Pro 190	Gly	Glu	
5	Gly Val	Arg 195	His	Leu	Lys	Glu	Thr 200	His	Arg	Ile	Thr	Leu 205	Phe	Gly	Arg	
10	Ala Glr 210		Glu	Ala	Ala	Phe 215	Thr	Ala	Ala	Gly	Met 220	Ser	Val	Glu	Tyr	
15	Leu Pro 225	o His	Ala	Ala	Thr 230	Asp	Arg	Gly	Leu	Phe 235	Val	Gly	Val	Gln	Ala 240	
20	<210> <211> <212> <213>	16 72 DNA Arti:	ficia	al												
	<220> <223>	prime	er													
25	<400> 16 ggggaattca gatctggtct agaggtcagc cggcgtggcg gcgcgtgagt tcctccagtc gcgggacgat ct															60
	gcgggacgat ct															72
30	<pre>gegggacgat ct  &lt;210&gt; 17 &lt;211&gt; 38 &lt;212&gt; DNA &lt;213&gt; Artificial</pre>															
35	<220> <223>	Prim														
40	<400> gggcata	17 atga	acga	ccgt	cc c	cgcc	gcgc	c at	gaag	gg						38
45	<210> <211> <212> <213>	18 50 DNA Arti	fici	al												
50	<220> <223> <400>	prim	er													
	cccctc		ggtc	actg	tg c	ccgg	ctgt	c gg	cggc	ggcc	ccg	cgca	tgg			50
55	<210><211><211><212><213>	19 52 DNA Arti	fici	al												
60	<220> <223>	prim														

```
<400> 19
     cccctctaga ggtcatgcgc gctccagttc cctgccgccc ggggaccgct tg
                                                                           52
 5
     <210>
            20
     <211>
            81
     <212>
            DNA
     <213> Artificial
10
     <220>
     <223> primer
     <400> 20
15
     gggtctagat cgattaatta aggaggacat tcatgcgcgt cctggtgacc ggaggtgcgg
                                                                            60
     gcttcatcgg ctcgcacttc a
                                                                            81
20
     <210> 21
     <211>
            40
     <212>
            DNA
     <213> Artificial
25
     <220>
     <223> primer
     <400> 21
     gggcatatgt acgaggcgg gttcgccgag ctttacgacc
                                                                            40
30
     <210> 22
     <211>
            40
     <212>
            DNA
35
     <213> Artificial
     <220>
     <223> primer
40
     <400> 22
     ggggtctaga ggtcatccgc gcacaccgac gaacaacccg
                                                                            40
     <210> 23
45
     <211> 38
     <212> DNA
     <213> Artificial
     <220>
50
     <223> primer
     <400> 23
     gggcatatgg cggcgagcac tacgacggag gggaatgt
                                                                           38
55
     <210> 24
     <211> 38
     <212> DNA
     <213> Artificial
50
     <220>
```

```
29/35
     <223> primer
     <400> 24
     gggtctagag gtcacgggtg gctcctgccg gccctcag
                                                                          38
5
     <210> 25
     <211> 22
     <212> DNA
10
     <213> Artificial
     <220>
     <223> primer
15
     <400> 25
     catcgtcaag gagttcgacg gt
                                                                          22
     <210> 26
20
     <211> 21
     <212> DNA
     <213> Artificial
     <220>
25
     <223> primer
     <400> 26
     gccagctcgg cgacgtccat c
                                                                          21
30
     <210> 27
     <211> 35
     <212> DNA
     <213> Artificial
35
     <220>
     <223> primer
     <400> 27
40
     gggcatatga gccccgcacc cgccaccgag gaccc
                                                                          35
     <210> 28
     <211> 42
45
     <212> DNA
     <213> Artificial
     <220>
     <223> primer
50
     <400> 28
                                                                           42
     ggtctagagg tcagttccgc ggtgcggtgg cgggcaggtc ac
55
     <210> 29
     <211> 41
     <212> DNA
     <213> Artificial
50
     <220>
     <223> primer
```

```
<400> 29
     gggcatatgc gtatcctgct gacgtcgttc gcgcacaaca c
                                                                             41
 5
     <210> 30
     <211> 44
<212> DNA
<213> Artificial
10
     <220>
     <223> primer
     <400> 30
15
     ggtctagagg tcaggcgcgg cggtgcgcgg cggtgaggcg ttcg
                                                                             44
     <210> 31
     <211> 39
20
     <212> DNA
     <213> Artificial
     <220>
     <223> primer
25
     <400> 31
     ggagatctgg cgcggcggtg cgcggcggtg aggcgttcg
                                                                             39
30
     <210> 32
     <211> 42
     <212> DNA
     <213> Artificial
35
     <220>
     <223> primer
     <400> 32
     gggcatatga acctcgaata cagcggcgac atcgcccggt tg
                                                                             42
40
     <210> 33
     <211> 44
     <212> DNA
45
     <213> Artificial
     <220>
     <223> primer
50
     <400> 33
     ggtctagagg tcaggcctgg acgccgacga agagtccgcg gtcg
                                                                             44
     <210> 34
     <211> 37
55
     <212> DNA
     <213> Artificial
     <220>
i0 <223> primer
```

```
<400> 34
     gggcatatga ctacctacgt ctgggactac ctggcgg
                                                                             37
5
     <210>
           35
     <211>
           40
     <212> DNA
     <213> Artificial
10
     <220>
     <223> primer
     <400> 35
     ggtctagagg tcagagcgtg gccagtacct cgtgcagggc
                                                                             40
15
     <210>
            36
     <211>
            41
     <212>
            DNA
20
     <213> Artificial
     <220>
     <223> primer
25
     <400> 36
     gggcatatgg tgaacgatcc gatgccgcgc ggcagtggca g
                                                                             41
     <210>
            37
30
     <211>
            43
     <212>
            DNA
     <213> Artificial
     <220>
35
     <223> primer
     <400> 37
     ggtctagagg tcaacctcca gagtgtttcg atggggtggt ggg
                                                                             43
10
     <210>
            38
     <211>
            39
     <212>
            DNA
     <213> Artificial
15
     <220>
     <223> primer
     <400> 38
50
                                                                              39
     gggcatatga agggcatcat cctggcgggc ggcagcggc
     <210>
            39
     <211>
            46
i5
     <212>
            DNA
     <213> Artificial
     <220>
     <223> primer
10
     <400>
            39
```

```
ggtctagagg tcatgcggcc ggtccggaca tgagggtctc cgccac
                                                                            46
     <210> 40
 5
     <211> 36
     <212> DNA
     <213> Artificial
     <220>
10
     <223> primer
     <400> 40
     gggcatatgc ggctgctggt caccggaggt gcgggc
                                                                           36
15
     <210> 41
     <211> 36
     <212> DNA
     <213> Artificial
20
     <220>
     <223> primer
     <400> 41
25
     ggtctagagg tcagtcggtg cgccgggcct cctgcg
                                                                           36
     <210> 42
     <211> 40
30
     <212> DNA
     <213> Artificial
     <220>
     <223> primer
35
     <400> 42
     gggcatatgt gtcctcctta attaatcgat gcgttcgtcc
                                                                           40
10
     <210> 43
     <211> 51
     <212> DNA
     <213> Artificial
15
     <220>
     <223> primer
     <400> 43
     ggagatotgg totagatogt gttcccctcc ctgcctcgtg gtccctcacg c
                                                                           51
0
     <210> 44
     <211> 36
     <212> DNA
5
     <213> Artificial
     <220>
     <223> primer
     <400> 44
     gggcatatga gcaccccttc cgcaccaccc gttccg
                                                                           36
```

PCT/GB2004/005001 33/35

```
<210> 45
     <211>
           40
 5
     <212> DNA
     <213> Artificial
     <220>
     <223> primer
10
     <400> 45
     ggtctagagg tcagtacagc gtgtgggcac acgccaccag
                                                                            40
15
     <210> 46
     <211> 37
     <212> DNA
     <213> Artificial
20
     <220>
     <223> primer
     <400> 46
     gggcatatga gcagttctgt cgaagctgag gcaagtg
                                                                           37
25
     <210> 47
     <211> 41
     <212> DNA
30
     <213> Artificial
     <220>
     <223> primer
15
     <400> 47
     ggtctagagg tcatcgcccc aacgcccaca agctatgcag g
                                                                           41
     <210> 48
:0
     <211> 33
     <212> DNA
     <213> Artificial
    <220>
.5
    <223> primer
    <400> 48
    cccatatgac cggagttcga ggtacgcggc ttg
                                                                           33
0
    <210> 49
    <211> 33
    <212> DNA
    <213> Artificial
5
    <220>
    <223> primer
    <400> 49
0
    gatactagtc cgccgaccgc acgtcgctga gcc
                                                                           33
```

```
<210>
            50
     <211>
            38
     <212>
            DNA
5
     <213> Artificial
     <220>
     <223>
           primer
10
     <400> 50
     tgcactagtg gccgggcgct cgacgtcatc gtcgacat
                                                                             38
     <210>
            51
15
     <211>
            36
     <212>
            DNA
     <213> Artificial
     <220>
20
     <223> primer
     <400> 51
     togatatogt gtoctgoggt ttoacotgoa acgotg
                                                                             36
25
     <210>
            52
     <211>
            36
     <212>
           DNA
     <213> Artificial
30
     <220>
     <223>
           primer
     <400> 52
35
     ggtctagact acgccgactg cctcggcgag gagccc
                                                                             36
     <210>
            53
     <211>
            36
10
     <212>
            DNA
     <213>
            Artificial
     <220>
     <223>
            primer
15
     <400> 53
     ggcatatgtt cgccgacgtg gaaacgacct gctgcg
                                                                             36
50
     <210>
            54
     <211>
            35
     <212>
            DNA
     <213>
            Artificial
55
     <220>
     <223>
            primer
     <400> 54
     ggaattcggc caggacgcgt ggctggtcac cggct
                                                                             35
50
```

35/35 <210> 55 <211> 42 <212> DNA <213> Artificial 5 <220> <223> primer <400> 55 10 ggtctagaaa gagcgtgagc aggctcttct acagccaggt ca 42 <210> 56 <211> 38 15 <212> DNA <213> Artificial <220> <223> primer 20 <400> 56 ggcatgcagg aaggagagaa ccacgatgac caccgacg 38 25 <210> 57 <211> 41 <212> DNA <213> Artificial 30 <220> <223> primer

ggtctagaca ccagccgtat cctttctcgg ttcctcttgt g

PCT/GB2004/005001

41

WO 2005/054265

<400> 57

35